

#11

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/555,093

DATE: 03/01/2002
 TIME: 15:04:43

Input Set : A:\09-555,093 sequence listing.txt
 Output Set: N:\CRF3\03012002\I555093.raw

4 <110> APPLICANT: Napier, Johnathan A.
 6 <120> TITLE OF INVENTION: Desaturase Genes and their Use
 9 <130> FILE REFERENCE: 000487.00001
 11 <140> CURRENT APPLICATION NUMBER: US 09/555,093
 12 <141> CURRENT FILING DATE: 2000-08-22
 14 <150> PRIOR APPLICATION NUMBER: UK 9724783.7
 15 <151> PRIOR FILING DATE: 1997-11-24
 17 <150> PRIOR APPLICATION NUMBER: PCT/GB98/03507
 18 <151> PRIOR FILING DATE: 1998-11-24
 20 <160> NUMBER OF SEQ ID NOS: 8
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1462
 26 <212> TYPE: DNA
 27 <213> ORGANISM: C. elegans
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (11)...(1340)
 33 <400> SEQUENCE: 1
 34 gctcaccaaa atg gtc gtc gac aag aat gcc tcc ggg ctt cga atg aag 49
 35 Met Val Val Asp Lys Asn Ala Ser Gly Leu Arg Met Lys
 36 1 5 10 97
 38 gtc gat ggc aaa tgg ctc tac ctt agc gag gaa ttg gtg aag aaa cat
 39 Val Asp Gly Lys Trp Leu Tyr Leu Ser Glu Glu Leu Val Lys Lys His
 40 15 20 25 145
 42 cca gga gga gct gtt att gaa caa tat aga aat tcg gat gct act cat
 43 Pro Gly Gly Ala Val Ile Glu Gln Tyr Arg Asn Ser Asp Ala Thr His
 44 30 35 40 45 193
 46 att ttc cac gct ttc cac gaa gga tct tct cag gct tat aag caa ctt
 47 Ile Phe His Ala Phe His Glu Gly Ser Ser Gln Ala Tyr Lys Gln Leu
 48 50 55 60 241
 50 gac ctt ctg aaa aag cac gga gag cac gat gaa ttc ctt gag aaa caa
 51 Asp Leu Leu Lys Lys His Gly Glu His Asp Glu Phe Leu Glu Lys Gln
 52 65 70 75 289
 54 ttg gaa aag aga ctt gac aaa gtt gat atc aat gta tca gca tat gat
 55 Leu Glu Lys Arg Leu Asp Lys Val Asp Ile Asn Val Ser Ala Tyr Asp
 56 80 85 90 337
 58 gtc agt gtt gca caa gaa aag aaa atg gtt gaa tca ttc gaa aaa cta
 59 Val Ser Val Ala Gln Glu Lys Lys Met Val Glu Ser Phe Glu Lys Leu
 60 95 100 105 385
 62 cga cag aag ctt cat gat gat gga tta atg aaa gca aat gaa aca tat
 63 Arg Gln Lys Leu His Asp Asp Gly Leu Met Lys Ala Asn Glu Thr Tyr
 64 110 115 120 125

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66	ttc	ctg	ttt	aaa	gcg	att	tca	aca	ctt	tca	att	atg	gca	ttt	gca	ttt	433
67	Phe	Leu	Phe	Lys	Ala	Ile	Ser	Thr	Leu	Ser	Ile	Met	Ala	Phe	Ala	Phe	
68										135							140
70	tat	ctt	cag	tat	ctt	gga	tgg	tat	att	act	tct	gca	tgt	tta	tta	gca	481
71	Tyr	Leu	Gln	Tyr	Leu	Gly	Trp	Tyr	Ile	Thr	Ser	Ala	Cys	Leu	Leu	Ala	
72										150							155
74	ctt	gca	tgg	caa	caa	ttc	gga	tgg	tta	aca	cat	gag	ttc	tgc	cat	caa	529
75	Leu	Ala	Trp	Gln	Gln	Phe	Gly	Trp	Leu	Thr	His	Glu	Phe	Cys	His	Gln	
76										165							170
78	cag	cca	aca	aag	aac	aga	cct	ttg	aat	gat	act	att	tct	ttg	ttc	ttt	577
79	Gln	Pro	Thr	Lys	Asn	Arg	Pro	Leu	Asn	Asp	Thr	Ile	Ser	Leu	Phe	Phe	
80										180							185
82	ggt	aat	ttc	tta	caa	gga	ttt	tca	aga	gat	tgg	tgg	aag	gac	aag	cat	625
83	Gly	Asn	Phe	Leu	Gln	Gly	Phe	Ser	Arg	Asp	Trp	Trp	Lys	Asp	Lys	His	
84	190									195							200
86	aac	act	cat	cac	gct	gcc	aca	aat	gta	att	gat	cat	gac	ggt	gat	atc	673
87	Asn	Thr	His	His	Ala	Ala	Thr	Asn	Val	Ile	Asp	His	Asp	Gly	Asp	Ile	
88										215							220
90	gac	ttg	gca	cca	ctt	ttc	gca	ttt	att	cca	gga	gat	ttg	tgc	aag	tat	721
91	Asp	Leu	Ala	Pro	Leu	Phe	Ala	Phe	Ile	Pro	Gly	Asp	Leu	Cys	Lys	Tyr	
92										225							230
94	aag	gcc	agc	ttt	gaa	aaa	gca	att	ctc	aag	att	gta	cca	tat	caa	cat	769
95	Lys	Ala	Ser	Phe	Glu	Lys	Ala	Ile	Leu	Lys	Ile	Val	Pro	Tyr	Gln	His	
96										240							245
98	ctc	tat	ttc	acc	gca	atg	ctt	cca	atg	ctc	cgt	ttc	tca	tgg	act	ggt	817
99	Leu	Tyr	Phe	Thr	Ala	Met	Leu	Pro	Met	Leu	Arg	Phe	Ser	Trp	Thr	Gly	
100										255							260
102	cag	tca	gtt	caa	tgg	gta	ttc	aaa	gag	aat	caa	atg	gag	tac	aag	gtc	865
103	Gln	Ser	Val	Gln	Trp	Val	Phe	Lys	Glu	Asn	Gln	Met	Glu	Tyr	Lys	Val	
104	270									275							280
106	tat	caa	aga	aat	gca	ttc	tgg	gag	caa	gca	aca	att	gtt	gga	cat	tgg	913
107	Tyr	Gln	Arg	Asn	Ala	Phe	Trp	Glu	Gln	Ala	Thr	Ile	Val	Gly	His	Trp	
108										290							295
110	gct	tgg	gta	ttc	tat	caa	ttg	ttc	tta	tta	cca	aca	tgg	cca	ctt	cgg	961
111	Ala	Trp	Val	Phe	Tyr	Gln	Leu	Phe	Leu	Leu	Pro	Thr	Trp	Pro	Leu	Arg	
112										305							310
114	gtt	gct	tat	ttc	att	att	tca	caa	atg	gga	gga	ggc	ctt	ttg	att	gct	1009
115	Val	Ala	Tyr	Phe	Ile	Ile	Ser	Gln	Met	Gly	Gly	Gly	Leu	Leu	Ile	Ala	
116										320							325
118	cac	gta	gtc	act	ttc	aac	cat	aac	tct	ggt	gat	aag	tat	cca	gcc	aat	1057
119	His	Val	Val	Thr	Phe	Asn	His	Asn	Ser	Val	Asp	Lys	Tyr	Pro	Ala	Asn	
120										335							340
122	tct	cga	att	tta	aac	aac	ttc	gcc	gct	ctt	caa	att	ttg	acc	aca	cgc	1105
123	Ser	Arg	Ile	Leu	Asn	Asn	Phe	Ala	Ala	Leu	Gln	Ile	Leu	Thr	Thr	Arg	
124	350									355							360
126	aac	atg	act	cca	tct	cca	ttc	att	gat	tgg	ctt	tgg	ggt	gga	ctc	aat	1153
127	Asn	Met	Thr	Pro	Ser	Pro	Phe	Ile	Asp	Trp	Leu	Trp	Gly	Gly	Leu	Asn	
128										370							375
130	tat	cag	atc	gag	cac	cac	ttg	ttc	cca	aca	atg	cca	cgt	tgc	aat	ctg	1201

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131 Tyr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg Cys Asn Leu
132          385          390          395          1249
134 aat gct tgc gtg aaa tat gtg aaa gaa tgg tgc aaa gag aat aat ctt
135 Asn Ala Cys Val Lys Tyr Val Lys Glu Trp Cys Lys Glu Asn Asn Leu
136          400          405          410          1297
138 cct tac ctc gtc gat gac tac ttt gac gga tat gca atg aat ttg caa
139 Pro Tyr Leu Val Asp Asp Tyr Phe Asp Gly Tyr Ala Met Asn Leu Gln
140          415          420          425          1340
142 caa ttg aaa aat atg gct gag cac att caa gct aaa gct gcc t
143 Gln Leu Lys Asn Met Ala Glu His Ile Gln Ala Lys Ala Ala
144 430          435          440          1400
146 aaacaatctg ggtgttcaaa aagttttttt ttgtttttta aatttaattc tttgaaatta 1460
147 tttgtttttc gtcattcttc ctccattccc ttttctgcta gaaataaaac cttgtttttc 1462
148 aa
150 <210> SEQ ID NO: 2
151 <211> LENGTH: 443
152 <212> TYPE: PRT
153 <213> ORGANISM: C. elegans
155 <400> SEQUENCE: 2
156 Met Val Val Asp Lys Asn Ala Ser Gly Leu Arg Met Lys Val Asp Gly
157 1          5          10          15
158 Lys Trp Leu Tyr Leu Ser Glu Glu Leu Val Lys Lys His Pro Gly Gly
159          20          25          30
160 Ala Val Ile Glu Gln Tyr Arg Asn Ser Asp Ala Thr His Ile Phe His
161          35          40          45
162 Ala Phe His Glu Gly Ser Ser Gln Ala Tyr Lys Gln Leu Asp Leu Leu
163          50          55          60
164 Lys Lys His Gly Glu His Asp Glu Phe Leu Glu Lys Gln Leu Glu Lys
165 65          70          75          80
166 Arg Leu Asp Lys Val Asp Ile Asn Val Ser Ala Tyr Asp Val Ser Val
167          85          90          95
168 Ala Gln Glu Lys Lys Met Val Glu Ser Phe Glu Lys Leu Arg Gln Lys
169          100          105          110
170 Leu His Asp Asp Gly Leu Met Lys Ala Asn Glu Thr Tyr Phe Leu Phe
171          115          120          125
172 Lys Ala Ile Ser Thr Leu Ser Ile Met Ala Phe Ala Phe Tyr Leu Gln
173          130          135          140
174 Tyr Leu Gly Trp Tyr Ile Thr Ser Ala Cys Leu Leu Ala Leu Ala Trp
175 145          150          155          160
176 Gln Gln Phe Gly Trp Leu Thr His Glu Phe Cys His Gln Gln Pro Thr
177          165          170          175
178 Lys Asn Arg Pro Leu Asn Asp Thr Ile Ser Leu Phe Phe Gly Asn Phe
179          180          185          190
180 Leu Gln Gly Phe Ser Arg Asp Trp Trp Lys Asp Lys His Asn Thr His
181          195          200          205
182 His Ala Ala Thr Asn Val Ile Asp His Asp Gly Asp Ile Asp Leu Ala
183          210          215          220
184 Pro Leu Phe Ala Phe Ile Pro Gly Asp Leu Cys Lys Tyr Lys Ala Ser
185 225          230          235          240

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```

186 Phe Glu Lys Ala Ile Leu Lys Ile Val Pro Tyr Gln His Leu Tyr Phe
187                               245                               250                               255
188 Thr Ala Met Leu Pro Met Leu Arg Phe Ser Trp Thr Gly Gln Ser Val
189                               260                               265                               270
190 Gln Trp Val Phe Lys Glu Asn Gln Met Glu Tyr Lys Val Tyr Gln Arg
191                               275                               280                               285
192 Asn Ala Phe Trp Glu Gln Ala Thr Ile Val Gly His Trp Ala Trp Val
193                               290                               295                               300
194 Phe Tyr Gln Leu Phe Leu Leu Pro Thr Trp Pro Leu Arg Val Ala Tyr
195 305                               310                               315                               320
196 Phe Ile Ile Ser Gln Met Gly Gly Gly Leu Leu Ile Ala His Val Val
197                               325                               330                               335
198 Thr Phe Asn His Asn Ser Val Asp Lys Tyr Pro Ala Asn Ser Arg Ile
199                               340                               345                               350
200 Leu Asn Asn Phe Ala Ala Leu Gln Ile Leu Thr Thr Arg Asn Met Thr
201                               355                               360                               365
202 Pro Ser Pro Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile
203 370                               375                               380
204 Glu His His Leu Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Ala Cys
205 385                               390                               395                               400
206 Val Lys Tyr Val Lys Glu Trp Cys Lys Glu Asn Asn Leu Pro Tyr Leu
207                               405                               410                               415
208 Val Asp Asp Tyr Phe Asp Gly Tyr Ala Met Asn Leu Gln Gln Leu Lys
209                               420                               425                               430
210 Asn Met Ala Glu His Ile Gln Ala Lys Ala Ala
211                               435                               440
213 <210> SEQ ID NO: 3
214 <211> LENGTH: 27
215 <212> TYPE: PRT
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: cytochrome b5 domain
221 <221> NAME/KEY: VARIANT
222 <222> LOCATION: (1)...(27)
223 <223> OTHER INFORMATION: Xaa = Any Amino Acid
225 <400> SEQUENCE: 3
W--> 226 His Pro Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
227 1                               5                               10                               15
W--> 228 Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His
229                               20                               25
231 <210> SEQ ID NO: 4
232 <211> LENGTH: 443
233 <212> TYPE: PRT
234 <213> ORGANISM: C. elegans
236 <400> SEQUENCE: 4
237 Met Val Val Asp Lys Asn Ala Ser Gly Leu Arg Met Lys Val Asp Gly
238 1                               5                               10                               15
239 Lys Trp Leu Tyr Leu Ser Glu Glu Leu Val Lys Lys His Pro Gly Gly
240                               20                               25                               30

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Input Set : A:\09-555,093 sequence listing.txt
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```

241 Ala Val Ile Glu Gln Tyr Arg Asn Ser Asp Ala Thr His Ile Phe His
242          35          40          45
243 Ala Phe His Glu Gly Ser Ser Gln Ala Tyr Lys Gln Leu Asp Leu Leu
244          50          55          60
245 Lys Lys His Gly Glu His Asp Glu Phe Leu Glu Lys Gln Leu Glu Lys
246 65          70          75          80
247 Arg Leu Asp Lys Val Asp Ile Asn Val Ser Ala Tyr Asp Val Ser Val
248          85          90          95
249 Ala Gln Glu Lys Lys Met Val Glu Ser Phe Glu Lys Leu Arg Gln Lys
250          100          105          110
251 Leu His Asp Asp Gly Leu Met Lys Ala Asn Glu Thr Tyr Phe Leu Phe
252          115          120          125
253 Lys Ala Ile Ser Thr Leu Ser Ile Met Ala Phe Ala Phe Tyr Leu Gln
254          130          135          140
255 Tyr Leu Gly Trp Tyr Ile Thr Ser Ala Cys Leu Leu Ala Leu Ala Trp
256 145          150          155          160
257 Gln Gln Phe Gly Trp Leu Thr His Glu Phe Cys His Gln Gln Pro Thr
258          165          170          175
259 Lys Asn Arg Pro Leu Asn Asp Thr Ile Ser Leu Phe Phe Gly Asn Phe
260          180          185          190
261 Leu Gln Gly Phe Ser Arg Asp Trp Trp Lys Asp Lys His Asn Thr His
262          195          200          205
263 His Ala Ala Thr Asn Val Ile Asp His Asp Gly Asp Ile Asp Leu Ala
264          210          215          220
265 Phe Leu Phe Ala Phe Ile Pro Gly Asp Leu Cys Lys Tyr Lys Ala Ser
266 225          230          235          240
267 Phe Glu Lys Ala Ile Leu Lys Ile Val Pro Tyr Gln His Leu Tyr Phe
268          245          250          255
269 Thr Ala Met Leu Pro Met Leu Arg Phe Ser Trp Thr Gly Gln Ser Val
270          260          265          270
271 Gln Trp Val Phe Lys Glu Asn Gln Met Glu Tyr Lys Val Tyr Gln Arg
272          275          280          285
273 Asn Ala Phe Trp Glu Gln Ala Thr Ile Val Gly His Trp Ala Trp Val
274          290          295          300
275 Phe Tyr Gln Leu Phe Leu Leu Pro Thr Trp Pro Leu Arg Val Ala Tyr
276 305          310          315          320
277 Phe Ile Ile Ser Gln Met Gly Gly Gly Leu Leu Ile Ala His Val Val
278          325          330          335
279 Thr Phe Asn His Asn Ser Val Asp Lys Tyr Pro Ala Asn Ser Arg Ile
280          340          345          350
281 Leu Asn Asn Phe Ala Ala Leu Gln Ile Leu Thr Thr Arg Asn Met Thr
282          355          360          365
283 Pro Ser Pro Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile
284          370          375          380
285 Glu His His Leu Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Ala Cys
286 385          390          395          400
287 Val Lys Tyr Val Lys Glu Trp Cys Lys Glu Asn Asn Leu Pro Tyr Leu
288          405          410          415
289 Val Asp Asp Tyr Phe Asp Gly Tyr Ala Met Asn Leu Gln Gln Leu Lys

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VERIFICATION SUMMARY

DATE: 03/01/2002

PATENT APPLICATION: US/09/555,093

TIME: 15:04:44

Input Set : A:\09-555,093 sequence listing.txt

Output Set: N:\CRF3\03012002\I555093.raw

L:226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3